Phyre^2

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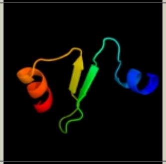
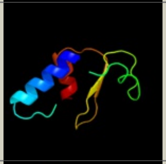
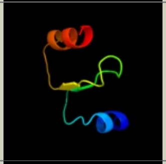
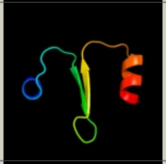
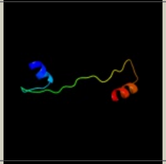
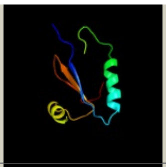
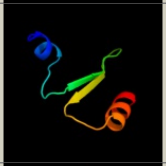
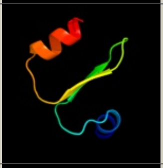
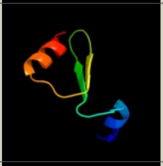
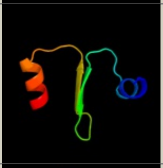
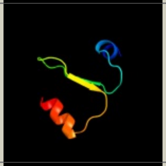
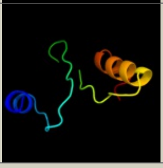
Detailed template information

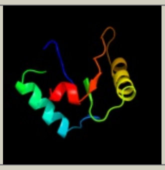
#	Template	Alignment Coverage	3D Model	Confidence	% i.d.	Template Information
1	d1hyua4	Alignment		95.4	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
2	c2vlvA_	Alignment		95.2	10	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin h isoform 2.; **PDBTitle:** crystal structure of barley thioredoxin h isoform 2 in2 partially radiation-reduced state
3	d1j08a2	Alignment		95.1	24	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
4	d1a8la2	Alignment		93.6	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
5	c1j08A_	Alignment		92.9	19	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**glutaredoxin-like protein; **PDBTitle:** crystal structure of glutaredoxin-like protein from2 pyrococcus horikoshii
6	c3gnjD_	Alignment		92.6	19	**PDB header:**structural genomics, unknown function **Chain:** D: **PDB Molecule:**thioredoxin domain protein; **PDBTitle:** the crystal structure of a thioredoxin-related protein from2 desulfitobacterium hafniense dcb
7	c1zypB_	Alignment		91.9	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**alkyl hydroperoxide reductase subunit f; **PDBTitle:** synchrotron reduced form of the n-terminal domain of2 salmonella typhimurium ahpf
8	c3emxB_	Alignment		91.8	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of thioredoxin from aeropyrum pernix
9	d1dbya_	Alignment		91.4	29	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
10	c2qsiB_	Alignment		91.4	19	**PDB header:**structural genomics, unknown function **Chain:** B: **PDB Molecule:**putative hydrogenase expression/formation protein hupg; **PDBTitle:** crystal structure of putative hydrogenase expression/formation protein2 hupg from rhodopseudomonas palustris cga009
11	c2vocA_	Alignment		91.2	19	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** thioredoxin a active site mutants form mixed disulfide2 dimers that resemble enzyme-substrate reaction3 intermediate

12	d1t4za_	Alignment		91.0	24	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**KaiB-like
13	c2pptA_	Alignment		90.6	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin-2; **PDBTitle:** crystal structure of thioredoxin-2
14	c2e0qA_	Alignment		90.2	19	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of k53e thioredoxin from sulfolobus2 tokodaii strain7
15	c2dj2A_	Alignment		90.2	12	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase a4; **PDBTitle:** the solution structure of the second thioredoxin domain of2 mouse protein disulfide-isomerase a4
16	c3p2aB_	Alignment		90.0	17	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**putative thioredoxin-like protein; **PDBTitle:** crystal structure of thioredoxin 2 from yersinia pestis
17	c2i4aA_	Alignment		89.9	24	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of thioredoxin from the acidophile2 acetobacter aceti
18	c3ul3A_	Alignment		89.8	5	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** structural insights into thioredoxin-2: a component of malaria2 parasite protein secretion machinery
19	d1ep7a_	Alignment		88.6	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
20	c1w89E_	Alignment		88.6	17	**PDB header:**electron transport **Chain:** E: **PDB Molecule:**thioredoxin; **PDBTitle:** structure of the reduced form of human thioredoxin 2
21	d2hfda1	Alignment		88.5	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**HyaE-like
22	d1r26a_	Alignment	not modelled	88.4	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
23	d1thxa_	Alignment	not modelled	88.3	26	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
24	c3p2aA_	Alignment	not modelled	87.9	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative thioredoxin-like protein; **PDBTitle:** crystal structure of thioredoxin 2 from yersinia pestis
25	c2o7kA_	Alignment	not modelled	87.7	21	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** s. aureus thioredoxin
26	c2l6dA_	Alignment	not modelled	87.5	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** solution structure of desulfothioredoxin from desulfovibrio vulgaris2 hildenborough in its reduced form
27	c3tcoA_	Alignment	not modelled	87.3	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin (trxa-1); **PDBTitle:** crystallographic and spectroscopic characterization of sulfolobus2 solfataricus trxa1 provide insights into the determinants of3 thioredoxin fold stability
						PDB header:oxidoreductase

28	c2vm2C_	Alignment	not modelled	87.1	8	**Chain:** C: **PDB Molecule:**thioredoxin h isoform 1.; **PDBTitle:** crystal structure of barley thioredoxin h isoform 12 crystallized using peg as precipitant
29	d1m7ta_	Alignment	not modelled	86.9	30	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
30	d2trxa_	Alignment	not modelled	86.8	33	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
31	c3hypB_	Alignment	not modelled	86.8	21	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of bacteroides fragilis trxp_s105g mutant
32	d1fb6a_	Alignment	not modelled	86.5	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
33	c2dj1A_	Alignment	not modelled	85.9	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase a4; **PDBTitle:** the solution structure of the first thioredoxin domain of2 mouse protein disulfide-isomerase a4
34	c3dmlA_	Alignment	not modelled	85.9	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative uncharacterized protein; **PDBTitle:** crystal structure of the periplasmic thioredoxin soxs from2 paracoccus pantotrophus (reduced form)
35	d1nhoa_	Alignment	not modelled	85.9	23	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
36	c2dizA_	Alignment	not modelled	85.6	19	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin domain-containing protein 5; **PDBTitle:** the solution structure of the third thioredoxin domain of2 human thioredoxin domain-containing protein 5
37	c2j23A_	Alignment	not modelled	85.5	20	**PDB header:**immune protein **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** cross-reactivity and crystal structure of malassezia2 sympodialis thioredoxin (mala s 13), a member of a new pan-3 allergen family
38	c3hz4A_	Alignment	not modelled	85.4	19	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of thioredoxin from methanosarcina mazei
39	d1xwaa_	Alignment	not modelled	85.3	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
40	c2xbqB_	Alignment	not modelled	85.2	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of reduced schistosoma mansoni2 thioredoxin pre-protein at 1.7 angstrom
41	d1nw2a_	Alignment	not modelled	85.2	26	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
42	c1t00A_	Alignment	not modelled	85.1	19	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** the structure of thioredoxin from s. coelicolor
43	c1x5eA_	Alignment	not modelled	85.0	12	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin domain containing protein 1; **PDBTitle:** the solution structure of the thioredoxin-like domain of2 human thioredoxin-related transmembrane protein
44	c2yzuA_	Alignment	not modelled	84.8	14	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure of oxidized thioredoxin from thermus thermophilus2 hb8
45	d1zmaa1	Alignment	not modelled	84.6	21	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
46	d1syra_	Alignment	not modelled	84.2	7	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
47	c2i1uA_	Alignment	not modelled	84.1	18	**PDB header:**electron transport **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** mycobacterium tuberculosis thioredoxin c
48	c2l5lA_	Alignment	not modelled	84.1	17	**PDB header:**transport protein **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** solution structure of thioredoxin from bacteroides vulgatus
49	c2f51B_	Alignment	not modelled	83.8	16	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**thioredoxin; **PDBTitle:** structure of trichomonas vaginalis thioredoxin
50	c2vimA_	Alignment	not modelled	83.6	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** x-ray structure of fasciola hepatica thioredoxin
51	c3d22A_	Alignment	not modelled	83.4	13	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin h-type; **PDBTitle:** crystal structure of a poplar thioredoxin h mutant,2 pttrxh4c61s
52	c3ewlA_	Alignment	not modelled	82.8	12	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized conserved protein bf1870; **PDBTitle:** crystal structure of conserved protein bf1870 of unknown function from2 bacteroides fragilis
53	c3idvA_	Alignment	not modelled	82.5	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase a4; **PDBTitle:** crystal structure of the a0a fragment of erp72
54	c3cxgA	Alignment	not modelled	81.6	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative thioredoxin;

54	c3cxgA_	Alignment	not modelled	81.6	17	**PDBTitle:** crystal structure of plasmodium falciparum thioredoxin, pfi0790w
55	c2kucA_	Alignment	not modelled	81.1	26	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**putative disulphide-isomerase; **PDBTitle:** solution structure of a putative disulphide-isomerase from bacteroides2 thetaiotaomicron
56	d1gh2a_	Alignment	not modelled	81.1	17	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
57	c1v98A_	Alignment	not modelled	81.1	29	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin; **PDBTitle:** crystal structure analysis of thioredoxin from thermus thermophilus
58	c2i9hA_	Alignment	not modelled	80.8	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thioredoxin i; **PDBTitle:** nmr solution structure of the reduced form of thioredoxin 12 from yeast (trx1)
59	c2wz9A_	Alignment	not modelled	80.6	19	**PDB header:**protein binding **Chain:** A: **PDB Molecule:**glutaredoxin-3; **PDBTitle:** crystal structure of the thioredoxin domain of human txnl2
60	d1a8la1	Alignment	not modelled	80.4	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
61	d1fo5a_	Alignment	not modelled	79.9	28	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
62	c1x5dA_	Alignment	not modelled	79.8	21	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase a6; **PDBTitle:** the solution structure of the second thioredoxin-like2 domain of human protein disulfide-isomerase a6
63	c3d6iB_	Alignment	not modelled	79.7	10	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**monothiol glutaredoxin-3; **PDBTitle:** structure of the thioredoxin-like domain of yeast2 glutaredoxin 3
64	c2l57A_	Alignment	not modelled	79.6	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized protein; **PDBTitle:** solution structure of an uncharacterized thioredoin-like protein from2 clostridium perfringens
65	c3g9bA_	Alignment	not modelled	78.9	30	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dolichyl-diphosphooligosaccharide-protein **PDBTitle:** crystal structure of reduced ost6l
66	d1ti3a_	Alignment	not modelled	78.4	7	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
67	d1v58a1	Alignment	not modelled	78.4	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbC/DsbG C-terminal domain-like
68	c3l9vE_	Alignment	not modelled	77.5	34	**PDB header:**oxidoreductase **Chain:** E: **PDB Molecule:**putative thiol-disulfide isomerase or thioredoxin; **PDBTitle:** crystal structure of salmonella enterica serovar typhimurium srga
69	d1oaza_	Alignment	not modelled	77.5	33	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
70	c2hyxA_	Alignment	not modelled	77.4	13	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**protein dipz; **PDBTitle:** structure of the c-terminal domain of dipz from mycobacterium2 tuberculosis
71	c2albA_	Alignment	not modelled	77.4	14	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase a3; **PDBTitle:** nmr structure of the n-terminal domain a of the2 glycoprotein chaperone erp57
72	c3feuA_	Alignment	not modelled	77.2	31	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative lipoprotein; **PDBTitle:** crystal structure of dsba-like thioredoxin domain vf_a0457 from vibrio2 fischeri
73	c3kzqE_	Alignment	not modelled	76.7	23	**PDB header:**structural genomics, unknown function **Chain:** E: **PDB Molecule:**putative uncharacterized protein vp2116; **PDBTitle:** the crystal structure of the protein with unknown function from vibrio2 parahaemolyticus rimd 2210633
74	c2dmlA_	Alignment	not modelled	76.5	17	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase a6; **PDBTitle:** the solution structure of the first thioredoxin domain of2 mouse protein disulfide-isomerase a6
75	c2p0oA_	Alignment	not modelled	76.4	10	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**hypothetical protein duf871; **PDBTitle:** crystal structure of a conserved protein from locus ef_2437 in2 enterococcus faecalis with an unknown function
76	c3gykC_	Alignment	not modelled	76.0	22	**PDB header:**oxidoreductase **Chain:** C: **PDB Molecule:**27kda outer membrane protein; **PDBTitle:** the crystal structure of a thioredoxin-like oxidoreductase from2 silicibacter pomeroyi dss-3
77	d1a8ya1	Alignment	not modelled	76.0	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Calsequestrin
78	c2ec4A_	Alignment	not modelled	75.8	15	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**fas-associated factor 1; **PDBTitle:** solution structure of the uas domain from human fas-2 associated factor 1
79	c3dvwA_	Alignment	not modelled	75.6	18	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsba; **PDBTitle:** crystal structure of reduced dsba1 from neisseria2 meningitidis
80	c2aytB_	Alignment	not modelled	75.4	15	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**glutaredoxin-like protein;

80	c2aytB_	Alignment	not modelled	75.4	15	**PDBTitle:** the crystal structure of a protein disulfide oxidoreductase from2 aquifex aeolicus
81	c2oe0B_	Alignment	not modelled	75.2	7	**PDB header:**electron transport **Chain:** B: **PDB Molecule:**thioredoxin-3; **PDBTitle:** crystal structure of mitochondrial thioredoxin 3 from2 saccharomyces cerevisiae
82	d1fvka_	Alignment	not modelled	75.2	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbA-like
83	c2znmA_	Alignment	not modelled	74.5	21	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsba; **PDBTitle:** oxidoreductase nmdsba3 from neisseria meningitidis
84	c3gl5A_	Alignment	not modelled	74.5	21	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative dsba oxidoreductase sco1869; **PDBTitle:** crystal structure of probable dsba oxidoreductase sco1869 from2 streptomyces coelicolor
85	d1zzoa1	Alignment	not modelled	74.2	15	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
86	d1f9ma_	Alignment	not modelled	72.2	24	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
87	c2hlsB_	Alignment	not modelled	71.3	18	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**protein disulfide oxidoreductase; **PDBTitle:** the crystal structure of a protein disulfide oxidoreductase from2 aeropyrum pernix k1
88	c3apsA_	Alignment	not modelled	71.1	9	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**dnaj homolog subfamily c member 10; **PDBTitle:** crystal structure of trx4 domain of erdj5
89	c3dxbE_	Alignment	not modelled	70.8	33	**PDB header:**splicing, transcription **Chain:** E: **PDB Molecule:**thioredoxin n-terminally fused to puf60(uhm); **PDBTitle:** structure of the uhm domain of puf60 fused to thioredoxin
90	c2in3A_	Alignment	not modelled	70.7	25	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**hypothetical protein; **PDBTitle:** crystal structure of a putative protein disulfide isomerase from2 nitrosomonas europaea
91	d1j08a1	Alignment	not modelled	70.4	20	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
92	d2fwha1	Alignment	not modelled	70.3	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
93	c2fgxA_	Alignment	not modelled	69.0	18	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**putative thioredoxin; **PDBTitle:** solution nmr structure of protein ne2328 from nitrosomonas2 europaea. northeast structural genomics consortium target3 net3.
94	d1meka_	Alignment	not modelled	68.3	16	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
95	c3h79A_	Alignment	not modelled	67.0	9	**PDB header:**unknown function **Chain:** A: **PDB Molecule:**thioredoxin-like protein; **PDBTitle:** crystal structure of trypanosoma cruzi thioredoxin-like hypothetical2 protein q4dv70
96	c3jr7A_	Alignment	not modelled	65.9	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**uncharacterized egv family protein cog1307; **PDBTitle:** the crystal structure of the protein of degv family cog1307 with2 unknown function from ruminococcus gnavus atcc 29149
97	d2b5ea4	Alignment	not modelled	65.3	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**PDI-like
98	d1mgpa_	Alignment	not modelled	65.2	12	**Fold:**DAK1/DegV-like **Superfamily:**DAK1/DegV-like **Family:**DegV-like
99	c1mgpA_	Alignment	not modelled	65.2	12	**PDB header:**lipid binding protein **Chain:** A: **PDB Molecule:**hypothetical protein tm841; **PDBTitle:** hypothetical protein tm841 from thermotoga maritima reveals2 fatty acid binding function
100	c3apqB_	Alignment	not modelled	64.4	19	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**dnaj homolog subfamily c member 10; **PDBTitle:** crystal structure of j-trx1 fragment of erdj5
101	c3hczA_	Alignment	not modelled	64.3	16	**PDB header:**structural genomics, unknown function **Chain:** A: **PDB Molecule:**possible thiol-disulfide isomerase; **PDBTitle:** the crystal structure of a domain of possible thiol-disulfide2 isomerase from cytophaga hutchinsonii atcc 33406.
102	c2dbcA_	Alignment	not modelled	63.4	24	**PDB header:**signaling protein **Chain:** A: **PDB Molecule:**unnamed protein product; **PDBTitle:** solution structure of the thioredoxin-like domain of2 phosducin-like protein 2(pdcl2)
103	d1xfla_	Alignment	not modelled	62.1	12	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
104	c1yzxB_	Alignment	not modelled	62.0	14	**PDB header:**transferase **Chain:** B: **PDB Molecule:**glutathione s-transferase kappa 1; **PDBTitle:** crystal structure of human kappa class glutathione2 transferase
105	c3kp8A_	Alignment	not modelled	61.9	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**vkorc1/thioredoxin domain protein; **PDBTitle:** the thioredoxin-like domain of a vkor homolog from2 synechococcus sp.

106	d2dlxa1	Alignment	not modelled	60.9	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**UAS domain
107	d1iloa_	Alignment	not modelled	60.0	22	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
108	d1wjka_	Alignment	not modelled	59.6	11	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Thioltransferase
109	c3h93A_	Alignment	not modelled	57.4	26	**PDB header:**transcription regulator **Chain:** A: **PDB Molecule:**thiol:disulfide interchange protein dsba; **PDBTitle:** crystal structure of pseudomonas aeruginosa dsba
110	c1x5cA_	Alignment	not modelled	57.3	11	**PDB header:**isomerase **Chain:** A: **PDB Molecule:**protein disulfide-isomerase; **PDBTitle:** the solution structure of the second thioredoxin-like2 domain of human protein disulfide-isomerase
111	d1z5ye1	Alignment	not modelled	57.1	14	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
112	c3gmfA_	Alignment	not modelled	56.4	14	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**protein-disulfide isomerase; **PDBTitle:** crystal structure of protein-disulfide isomerase from novosphingobium2 aromaticivorans
113	c3qdnA_	Alignment	not modelled	56.2	12	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**putative thioredoxin protein; **PDBTitle:** putative thioredoxin protein from salmonella typhimurium
114	c3fysA_	Alignment	not modelled	55.7	23	**PDB header:**fatty acid-binding protein **Chain:** A: **PDB Molecule:**protein degv; **PDBTitle:** crystal structure of degv, a fatty acid binding protein2 from bacillus subtilis
115	c1xbsA_	Alignment	not modelled	55.6	14	**PDB header:**transcription, cell cycle **Chain:** A: **PDB Molecule:**dim1-like protein; **PDBTitle:** crystal structure of human dim2: a dim1-like protein
116	c2dunA_	Alignment		55.3	13	**PDB header:**transferase **Chain:** A: **PDB Molecule:**dna polymerase mu; **PDBTitle:** solution structure of brct domain of dna polymerase mu
117	c3ghaA_	Alignment	not modelled	53.7	17	**PDB header:**oxidoreductase **Chain:** A: **PDB Molecule:**disulfide bond formation protein d; **PDBTitle:** crystal structure of etda-treated bdbd (reduced)
118	d1o73a_	Alignment	not modelled	52.2	13	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**Glutathione peroxidase-like
119	d1eeja1	Alignment	not modelled	51.1	18	**Fold:**Thioredoxin fold **Superfamily:**Thioredoxin-like **Family:**DsbC/DsbG C-terminal domain-like
120	c2remB_	Alignment	not modelled	49.9	14	**PDB header:**oxidoreductase **Chain:** B: **PDB Molecule:**disulfide oxidoreductase; **PDBTitle:** crystal structure of oxidoreductase dsba from xylella2 fastidiosa